



#7

-1-

SEQUENCE LISTING

<110> Yamamoto, Satoshi
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<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE
GENE AS AN INDICATOR

<130> 12817-004001

<140> US 09/823,823

<141> 2001-03-30

<150> US 09/208,688

<151> 1998-12-10

<150> JP 97/343316

<151> 1997-12-12

<160> 80

<170> PatentIn version 2.0

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<212> DNA

<213> Bacteroides vulgatus

<220>

<221> CDS

<222> (1)...(1212)

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tct	tgt	gtg	aac	gcc	ttg	tct	act	cac	atg	acc	aca	cag	gta	ttc	cgc	96
Ser	Cys	Val	Asn	Ala	Leu	Ser	Thr	His	Met	Thr	Thr	Gln	Val	Phe	Arg	
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ggt	ggc	aag	atc	tac	cag	cag	gaa	tac	agc	tgc	gga	cat	cct	ttg	tat	144
Gly	Gly	Lys	Ile	Tyr	Gln	Gln	Glu	Tyr	Ser	Cys	Gly	His	Pro	Leu	Tyr	
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tct	gta	aaa	gaa	gta	gga	aca	gct	gat	att	acc	gga	aca	aaa	cag	act	192
Ser	Val	Lys	Glu	Val	Gly	Thr	Ala	Asp	Ile	Thr	Gly	Thr	Lys	Gln	Thr	
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ttc	tgg	cgc	gat	gat	acc	atc	ttc	act	gtt	acc	gaa	tat	aag	ttt	gac	240
Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp	
65					70				75					80		

att	cta	cag	gca	cgt	atg	cgt	gaa	ttg	gcc	tac	ttg	aac	aaa	ggt	atc	288
Ile	Leu	Gln	Ala	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly	Ile	
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acc att	aca	ctg	acc	gac	cgc	cgg	atc	aaa	gaa	gaa	gat	ggc	agc	ttc	336
Thr Ile	Ser	Leu	Thr	Asp	Arg	Arg	Ile	Lys	Glu	Glu	Asp	Gly	Ser	Phe	
		100					105					110			
aag aaa	gaa	ata	ttc	cat	tcg	gac	gaa	gga	gtg	aaa	gag	ttt	gta	cgt	384
Lys Lys	Glu	Ile	Phe	His	Ser	Asp	Glu	Gly	Val	Lys	Glu	Phe	Val	Arg	
	115					120					125				
ttc ctg	aac	cgt	aac	aac	gaa	gcg	ctg	att	aat	gat	gtc	att	tat	ctg	432
Phe Leu	Asn	Arg	Asn	Asn	Glu	Ala	Leu	Ile	Asn	Asp	Val	Ile	Tyr	Leu	
	130				135					140					
aat acc	gaa	aaa	aac	aac	gaa	gcg	ctg	att	gaa	tgt	gcc	atc	atg	tac	aat
Asn Thr	Glu	Lys	Asn	Asn	Thr	Pro	Ile	Glu	Cys	Ala	Ile	Met	Tyr	Asn	
145				150					155					160	480
aca ggc	tat	cgt	gaa	agc	ctg	cat	tcg	tat	gta	aac	aac	atc	aat	aca	528
Thr Gly	Tyr	Arg	Glu	Ser	Leu	His	Ser	Tyr	Val	Asn	Asn	Ile	Asn	Thr	
			165					170					175		
ata gaa	ggc	ggt	aca	cac	gag	gcc	ggt	ttc	cgc	agc	gca	tta	acc	cgt	576
Ile Glu	Gly	Gly	Thr	His	Glu	Ala	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Arg	
		180					185					190			
gta ctg	aag	aaa	tat	gcg	gaa	gat	acc	aaa	gca	ctg	gaa	aaa	gca	aaa	624
Val Leu	Lys	Lys	Tyr	Ala	Glu	Asp	Thr	Lys	Ala	Leu	Glu	Lys	Ala	Lys	
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gtc gag	att	tcg	gga	gag	gac	ttc	cgc	gaa	ggc	ttg	att	gcc	gtc	att	672
Val Glu	Ile	Ser	Gly	Glu	Asp	Phe	Arg	Glu	Gly	Leu	Ile	Ala	Val	Ile	
	210				215					220					
tca gtg	aaa	gta	gcc	gag	ccg	cag	ttc	gaa	gga	cag	acc	aag	acc	aag	720
Ser Val	Lys	Val	Ala	Glu	Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys	
225				230					235					240	
ctg ggc	aac	agc	gaa	gtg	agt	ggt	gcc	gtg	aac	caa	gct	gta	ggc	gaa	768
Leu Gly	Asn	Ser	Glu	Val	Ser	Gly	Ala	Val	Asn	Gln	Ala	Val	Gly	Glu	
		245					250						255		
gcg ctt	aca	tat	tat	ctg	gaa	gaa	cat	ccg	aaa	gaa	gca	aaa	cag	att	816
Ala Leu	Thr	Tyr	Tyr	Leu	Glu	Glu	His	Pro	Lys	Glu	Ala	Lys	Gln	Ile	
		260					265					270			
gtt gac	aaa	gtg	atc	ctg	gct	gca	aca	gcg	cgt	atc	gcc	gca	cgc	aag	864
Val Asp	Lys	Val	Ile	Leu	Ala	Ala	Thr	Ala	Arg	Ile	Ala	Ala	Arg	Lys	
	275					280					285				
gca cgt	gaa	tct	gtt	caa	aga	aag	agt	ccg	atg	ggc	ggt	ggc	gga	ctg	912
Ala Arg	Glu	Ser	Val	Gln	Arg	Lys	Ser	Pro	Met	Gly	Gly	Gly	Gly	Leu	
	290				295					300					
ccg ggc	aaa	ctg	gcc	gac	tgc	tcg	agc	cgt	aat	ccg	gag	gaa	tgt	gaa	960
Pro Gly	Lys	Leu	Ala	Asp	Cys	Ser	Ser	Arg	Asn	Pro	Glu	Glu	Cys	Glu	
305				310					315					320	
cta ttc	ctg	gtc	gag	ggt	gac	tcg	gca	ggt	ggt	tct	gcc	aag	caa	gga	1008
Leu Phe	Leu	Val	Glu	Gly	Asp	Ser	Ala	Gly	Gly	Ser	Ala	Lys	Gln	Gly	
			325					330					335		

cgt agc ~~agt~~ gcc ttc cag gca att cta cct ttg agg ggt aaa atc ctg 1056
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
 340 345 350

aat gtg gaa aaa gcg atg tgg cac aag gct ttt gaa agc gat gag gtc 1104
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
 355 360 365

aat aat atc atc acc gcc ctg ggt gtc cgt ttc ggt gtg gac gga aat 1152
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
 370 375 380

gat gac agc aaa aaa gcg aac atc gac aag ctg cgt tat cac aaa gtg 1200
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 385 390 395 400

gtg atc atg acc
 Val Ile Met Thr

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 <212> PRT
 <213> Bacteroides vulgatus

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 Gly Gly Lys Ile Tyr Gln Gln Glu Tyr Ser Cys Gly His Pro Leu Tyr
 35 40 45
 Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr
 50 55 60
 Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp
 65 70 75 80
 Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile
 85 90 95
 Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe
 100 105 110
 Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg
 115 120 125
 Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu
 130 135 140
 Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn
 145 150 155 160
 Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr
 165 170 175
 Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg
 180 185 190
 Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys
 195 200 205
 Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile
 210 215 220
 Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys
 225 230 235 240
 Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu
 245 250 255
 Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile
 260 265 270
 Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys
 275 280 285

Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu
 290 295 300
 Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
 305 310 315 320
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
 325 330 335
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
 340 345 350
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
 355 360 365
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
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 Val Ile Met Thr

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 <213> Mycobacterium simiae

<220>
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 <222> (1)...(1263)

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 gtg tcg gtg gtc aac gcc ctg tcc acc cgc ctg gaa gtc aac gtc aag 96
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys
 20 25 30
 cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc 144
 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
 35 40 45
 acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg 192
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag 240
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg 288
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat 336
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag 384
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
 115 120 125
 gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac 432
 Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140

tac ccg aggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa	480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg	528
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly	
165 170 175	
cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg	576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	
gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac	624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc	672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac	720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225 230 235 240	
gac atc cga gaa ggc ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag	768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	
245 250 255	
ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc	816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val	
260 265 270	
aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc	864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe	
275 280 285	
gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg	912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser	
290 295 300	
tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg	960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg	
305 310 315 320	
cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat	1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp	
325 330 335	
tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt	1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly	
340 345 350	
gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag	1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln	
355 360 365	
gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc	1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg	
370 375 380	

atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400

ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac 1248
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415

cac aag atc gtg ttg 1263
 His Lys Ile Val Leu
 420

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 <211> 421
 <212> PRT
 <213> Mycobacterium simiae

<400> 4
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 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
 115 120 125
 Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
 405 410 415
 His Lys Ile Val Leu
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 <213> Chitinophaga pinensis

<220>
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 <222> (1)...(660)

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 gat aag aac aaa atg ttc gaa aaa acc aag atc gaa gta aca ggt gat 96
 Asp Lys Asn Lys Met Phe Glu Lys Thr Lys Ile Glu Val Thr Gly Asp
 20 25 30
 gac ttc cgt gaa ggt ctg agc gct atc atc agc gta aaa gta cct gaa 144
 Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu
 35 40 45
 cca cag ttc gaa ggc cag acc aaa acc aaa ctc ggt aac tcc gat gta 192
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val
 50 55 60
 atg ggg gtt gtg gac agt tcc gta gca gcc gta ctg gat gcc tac ctg 240
 Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu
 65 70 75 80
 gaa gaa cat ccc cgc gaa gcc aag atc att atc aat aaa gtg gta ctg 288
 Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu
 85 90 95
 gca gca cag gcg cgt gaa gca gcc cgt aaa gca cgc cag atg gta cag 336
 Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln
 100 105 110
 cgt aag agc gta ctg agt gga agc ggc ttg oct ggt aaa ctg gct gac 384
 Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp
 115 120 125
 tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt 432
 Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly
 130 135 140
 gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag 480
 Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln
 145 150 155 160

gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg	528
Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met	
165 170 175	
gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca	576
Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala	
180 185 190	
ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc	624
Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu	
195 200 205	
tcc aaa ctg cgc tat cac aaa ctg atc atc atg acg	660
Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr	
210 215 220	

<210> 6
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 <212> PRT
 <213> Chitinophaga pinensis

<400> 6

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20 25 30	
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35 40 45	
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val	
50 55 60	
Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu	
65 70 75 80	
Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu	
85 90 95	
Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln	
100 105 110	
Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp	
115 120 125	
Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly	
130 135 140	
Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln	
145 150 155 160	
Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met	
165 170 175	
Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala	
180 185 190	
Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu	
195 200 205	
Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr	
210 215 220	

<210> 7
 <211> 537
 <212> DNA
 <213> Flavobacterium aquatile

<220>
 <221> CDS
 <222> (1)...(537)

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 Ser Cys Val Asn Ala Leu Ser Asp Asn Leu Lys Ala Thr Val Phe Arg
 20 25 30

gac gga aaa gtg tac gag caa gaa tat gaa aaa ggt aaa gca atg tat 144
 Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
 35 40 45

ccg gtt aag caa gtt ggt gaa aca aca aag cga gga aca atg gtt act 192
 Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
 50 55 60

ttt cat cct gat aaa acc att ttt act caa aca att gag tat tct tat 240
 Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
 65 70 75 80

gat aca ctt gca gca cgt atg cgt gaa tta tct ttc ctg aat aaa gga 288
 Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
 85 90 95

att aca atc aca ctt aca gat aaa aga cat act aaa gac aac ggc gat 336
 Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
 100 105 110

ttt gaa ggt gaa gtt ttt cat tct aaa gaa ggg ctt aaa gaa ttc gtt 384
 Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
 115 120 125

cga ttt tta gat gct ggt aga gaa cca att att tct cac gta ata agc 432
 Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
 130 135 140

atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480
 Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
 145 150 155 160

aat aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528
 Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn
 165 170 175

acg cac gaa 537
 Thr His Glu

<210> 8
 <211> 179
 <212> PRT
 <213> Flavobacterium aquatile

<400> 8
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 Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
 35 40 45

Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
 50 55 60
 Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
 65 70 75 80
 Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
 85 90 95
 Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
 100 105 110
 Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
 115 120 125
 Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
 130 135 140
 Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
 145 150 155 160
 Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn
 165 170 175
 Thr His Glu

<210> 9
 <211> 783
 <212> DNA
 <213> Mycobacterium asiaticum

<220>
 <221> CDS
 <222> (1)...(783)

<400> 9
 ggc gag aac agc ggc tac acc gtc agc ggt ggg ttg cac gga gtg ggc 48
 Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
 1 5 10 15
 gtg tcg gtg gtc aac gcg ctg tcc acc cgc ctg gag gtc acc atc aag 96
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
 20 25 30
 cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga 144
 Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
 35 40 45
 acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg 192
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag 240
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc 288
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac 336
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag 384
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
 115 120 125

gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac 432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140

tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag 480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160

agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc 528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
165 170 175

cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc 576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190

gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac 624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205

gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc 672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220

aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac 720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225 230 235 240

gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag 768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
245 250 255

cca cag ttc gaa ggc 783
Pro Gln Phe Glu Gly
260

<210> 10
<211> 261
<212> PRT
<213> Mycobacterium asiaticum

<400> 10
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
20 25 30
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
115 120 125
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160

Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly
 260

<210> 11
 <211> 195
 <212> DNA
 <213> Cytophaga lytica

<220>
 <221> CDS
 <222> (1)...(195)

<400> 11
 agc cac att gaa act tta att ctt aca ttc ttc ttc cgt ttt atg cga 48
 Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg
 1 5 10 15
 gaa cta ata gaa ggc gga cac gtt tac ata gca aca cca cct tta tat 96
 Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr
 20 25 30
 tta gtt aaa aaa gga act aaa aag cgt tat gct tgg aat gat aaa gaa 144
 Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu
 35 40 45
 cga gat gaa ata gca gat agc ttt aat ggt agt gta ggt atc caa aga 192
 Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg
 50 55 60
 tat 195
 Tyr
 65

<210> 12
 <211> 65
 <212> PRT
 <213> Cytophaga lytica

<400> 12
 Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg
 1 5 10 15
 Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr
 20 25 30
 Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu
 35 40 45
 Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg
 50 55 60
 Tyr
 65

<210> 13
 <211> 1170
 <212> DNA
 <213> Synechococcus sp.

<220>
 <221> CDS
 <222> (1)...(1170)

<400> 13
 gtg gtg gac aac gcc gtc gac aaa gcc ttg gcg ggc tac tgc aat acc 48
 Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr
 1 5 10 15
 att gat gtt cgt ctg ctc aaa gac ggc tcc tgc caa gtc acc gat aac 96
 Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn
 20 25 30
 ggt cgc ggc att ccc aca gat att cac ccc caa acc ggg aag tct gct 144
 Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala
 35 40 45
 ctc gaa acc gtg ctg acg att ctg cac gcg ggc ggc aag ttt ggc ggt 192
 Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly
 50 55 60
 ggc ggt tat aag gtg tcg ggg ggt ctg cac ggc gtc ggt gtg tct gtc 240
 Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser Val
 65 70 75 80
 gtc aac gcc ctc tca gaa tat gtc gaa gtc acc gtg tgg cgg gaa ggc 288
 Val Asn Ala Leu Ser Glu Tyr Val Glu Val Thr Val Trp Arg Glu Gly
 85 90 95
 aaa acc cac caa cag cgc ttt gaa cag ggc aac ccg atc ggg gag ttg 336
 Lys Thr His Gln Gln Arg Phe Glu Gln Gly Asn Pro Ile Gly Glu Leu
 100 105 110
 caa gtt gcc ccg gat gcc gac gat cgc cgc ggg aca caa gtt cgt ttc 384
 Gln Val Ala Pro Asp Ala Asp Arg Arg Gly Thr Gln Val Arg Phe
 115 120 125
 aaa cca gac gcc acg atc ttt tct gaa aca acc gag ttc gat tac ggc 432
 Lys Pro Asp Ala Thr Ile Phe Ser Glu Thr Thr Glu Phe Asp Tyr Gly
 130 135 140
 acc cta gca agc cga ttg aag gag cta gcc tat ctg aat gcg ggc gtc 480
 Thr Leu Ala Ser Arg Leu Lys Glu Leu Ala Tyr Leu Asn Ala Gly Val
 145 150 155 160
 cgc atc gac ttt acc gat gag cgg ctg cag ctc acc aag aat cac gag 528
 Arg Ile Asp Phe Thr Asp Glu Arg Leu Gln Leu Thr Lys Asn His Glu
 165 170 175
 ccc cat caa gaa acc tat tac ttt gaa ggc ggt att cgc gaa tac gtc 576
 Pro His Gln Glu Thr Tyr Tyr Phe Glu Gly Gly Ile Arg Glu Tyr Val
 180 185 190
 gcc tac atg aat acc gat aaa cag gcg ctg cac tca gag att atc ttt 624
 Ala Tyr Met Asn Thr Asp Lys Gln Ala Leu His Ser Glu Ile Ile Phe
 195 200 205

gtg	caa	tcc	gaa	aaa	gat	ggc	gtc	caa	gtt	gaa	gct	gca	ttg	caa	tgg	672
Val	Gln	Ser	Glu	Lys	Asp	Gly	Val	Gln	Val	Glu	Ala	Ala	Leu	Gln	Trp	
	210					215					220					
tgc	gtt	gac	gcc	tac	agc	gac	aac	att	ctg	ggc	ttt	gcc	aac	aac	atc	720
Cys	Val	Asp	Ala	Tyr	Ser	Asp	Asn	Ile	Leu	Gly	Phe	Ala	Asn	Asn	Ile	
225					230					235					240	
cgc	acg	att	gac	ggc	ggc	acc	cat	att	gag	ggg	ctc	aaa	act	gtt	ctg	768
Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Glu	Gly	Leu	Lys	Thr	Val	Leu	
				245					250					255		
acg	cgg	acg	atg	aac	acg	atc	gcc	cgc	aaa	cgg	aat	aaa	cgc	aag	gat	816
Thr	Arg	Thr	Met	Asn	Thr	Ile	Ala	Arg	Lys	Arg	Asn	Lys	Arg	Lys	Asp	
			260					265					270			
gcc	gac	aat	aac	ctg	tcg	ggc	gag	aat	att	cgc	gaa	ggg	tta	aca	gcg	864
Ala	Asp	Asn	Asn	Leu	Ser	Gly	Glu	Asn	Ile	Arg	Glu	Gly	Leu	Thr	Ala	
		275					280					285				
atc	gtt	tcg	gtc	aaa	gtt	ccg	gat	ccg	gaa	ttt	gaa	ggg	caa	acc	aaa	912
Ile	Val	Ser	Val	Lys	Val	Pro	Asp	Pro	Glu	Phe	Glu	Gly	Gln	Thr	Lys	
	290					295					300					
aca	aag	ctc	ggc	aat	acc	gaa	gtt	cgc	ggc	atc	gtc	gat	acg	ctc	gtg	960
Thr	Lys	Leu	Gly	Asn		Glu	Val	Arg	Gly	Ile	Val	Asp	Thr	Leu	Val	
305				310					315					320		
ggc	gaa	acg	ttg	acg	gaa	tat	ctg	gaa	ttc	cat	ccc	agc	gtt	gcc	gat	1008
Gly	Glu	Thr	Leu	Thr	Glu	Tyr	Leu	Glu	Phe	His	Pro	Ser	Val	Ala	Asp	
				325					330					335		
ttg	atc	ctc	gaa	aaa	gcg	att	caa	gcc	ttt	aat	gcg	gct	gag	gca	gcg	1056
Leu	Ile	Leu	Glu	Lys	Ala	Ile	Gln	Ala	Phe	Asn	Ala	Ala	Glu	Ala	Ala	
			340					345					350			
cga	cgg	gca	cgg	gaa	ttg	gtg	cgt	cgc	aaa	tca	gtg	ctg	gaa	tct	tcg	1104
Arg	Arg	Ala	Arg	Glu	Leu	Val	Arg	Arg	Lys	Ser	Val	Leu	Glu	Ser	Ser	
		355					360					365				
aca	ttg	ccc	ggt	aaa	tta	gca	gac	tgt	tcc	agt	cgc	gat	ccc	ggt	gaa	1152
Thr	Leu	Pro	Gly	Lys	Leu	Ala	Asp	Cys	Ser	Ser	Arg	Asp	Pro	Gly	Glu	
	370					375					380					
tct	gaa	atc	ttc	atc	gtg											1170
Ser	Glu	Ile	Phe	Ile	Val											
385					390											

<210> 14
 <211> 390
 <212> PRT
 <213> Synechoccus sp.

<400> 14
 Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr
 1 5 10 15
 Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn
 20 25 30
 Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala
 35 40 45
 Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly
 50 55 60

Gly	Gly	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser	Val
65					70					75					80
Val	Asn	Ala	Leu	Ser	Glu	Tyr	Val	Glu	Val	Thr	Val	Trp	Arg	Glu	Gly
				85					90					95	
Lys	Thr	His	Gln	Gln	Arg	Phe	Glu	Gln	Gly	Asn	Pro	Ile	Gly	Glu	Leu
			100					105					110		
Gln	Val	Ala	Pro	Asp	Ala	Asp	Asp	Arg	Arg	Gly	Thr	Gln	Val	Arg	Phe
		115				120						125			
Lys	Pro	Asp	Ala	Thr	Ile	Phe	Ser	Glu	Thr	Thr	Glu	Phe	Asp	Tyr	Gly
	130					135					140				
Thr	Leu	Ala	Ser	Arg	Leu	Lys	Glu	Leu	Ala	Tyr	Leu	Asn	Ala	Gly	Val
	145				150					155					160
Arg	Ile	Asp	Phe	Thr	Asp	Glu	Arg	Leu	Gln	Leu	Thr	Lys	Asn	His	Glu
			165						170					175	
Pro	His	Gln	Glu	Thr	Tyr	Tyr	Phe	Glu	Gly	Gly	Ile	Arg	Glu	Tyr	Val
		180						185					190		
Ala	Tyr	Met	Asn	Thr	Asp	Lys	Gln	Ala	Leu	His	Ser	Glu	Ile	Ile	Phe
		195					200					205			
Val	Gln	Ser	Glu	Lys	Asp	Gly	Val	Gln	Val	Glu	Ala	Ala	Leu	Gln	Trp
	210					215				220					
Cys	Val	Asp	Ala	Tyr	Ser	Asp	Asn	Ile	Leu	Gly	Phe	Ala	Asn	Asn	Ile
	225				230					235					240
Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Glu	Gly	Leu	Lys	Thr	Val	Leu
			245						250					255	
Thr	Arg	Thr	Met	Asn	Thr	Ile	Ala	Arg	Lys	Arg	Asn	Lys	Arg	Lys	Asp
		260						265					270		
Ala	Asp	Asn	Asn	Leu	Ser	Gly	Glu	Asn	Ile	Arg	Glu	Gly	Leu	Thr	Ala
		275					280					285			
Ile	Val	Ser	Val	Lys	Val	Pro	Asp	Pro	Glu	Phe	Glu	Gly	Gln	Thr	Lys
	290					295					300				
Thr	Lys	Leu	Gly	Asn	Thr	Glu	Val	Arg	Gly	Ile	Val	Asp	Thr	Leu	Val
	305				310					315					320
Gly	Glu	Thr	Leu	Thr	Glu	Tyr	Leu	Glu	Phe	His	Pro	Ser	Val	Ala	Asp
			325						330					335	
Leu	Ile	Leu	Glu	Lys	Ala	Ile	Gln	Ala	Phe	Asn	Ala	Ala	Glu	Ala	Ala
			340					345					350		
Arg	Arg	Ala	Arg	Glu	Leu	Val	Arg	Arg	Lys	Ser	Val	Leu	Glu	Ser	Ser
		355					360					365			
Thr	Leu	Pro	Gly	Lys	Leu	Ala	Asp	Cys	Ser	Ser	Arg	Asp	Pro	Gly	Glu
	370					375					380				
Ser	Glu	Ile	Phe	Ile	Val										
385					390										

<210> 15
 <211> 696
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1)...(696)

<400> 15																	
cag	aac	agc	tac	aag	gtc	tcg	ggc	ggt	ctg	cac	ggc	gtg	ggc	gtc	tcg		48
Gln	Asn	Ser	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser		
1				5					10					15			
gtc	gtg	aac	gcc	ctg	tcg	gat	tgg	ctg	gag	ctg	ctg	atc	cac	cgc	aac		96
Val	Val	Asn	Ala	Leu	Ser	Asp	Trp	Leu	Glu	Leu	Leu	Ile	His	Arg	Asn		
			20					25					30				

ggc aag gtc cac cag atg cgc ttc gag cgc ggc gac gcg gtc acc tcg 144
 Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser
 35 40 45

ctg aag gtc acc ggc gac tcg ccc gtg cgg acc gag ggc ccc aag gcc 192
 Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala
 50 55 60

ggc gag acc ctg acc ggt acg gaa gtt acg ttc ttt ccg tcg aag gac 240
 Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp
 65 70 75 80

acc ttc gcc ttc atc gaa ttc gac cgg aag acg ctg gag cac cgc ctg 288
 Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu
 85 90 95

cgc gag ctg gcc ttc ctg aac tcg ggc gtg acg atc tgg ttc aag gac 336
 Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp
 100 105 110

cat cgc gac gtc gag ccg tgg gaa gag aag ctg ttc tac gag ggc ggc 384
 His Arg Asp Val Glu Pro Trp Glu Lys Leu Phe Tyr Glu Gly Gly
 115 120 125

atc gag gcc ttc gtg cgc cac ctc gac aag gcc aag acg ccg ctg ctg 432
 Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu
 130 135 140

aag gcc ccg atc gcc gtc aag ggc gtc aag gac aag gtc gag atc gac 480
 Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp
 145 150 155 160

ctg gcc ctg tgg tgg aac gac agc tac cac gag cag atg ctg tgc ttc 528
 Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe
 165 170 175

acc aac aac atc ccg cag cgg gat ggc ggc acg cac ctg tcg gcc ttt 576
 Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe
 180 185 190

cgc gcg gcc ctg acc cgg atc atc acc agc tac gcc gag agc tcc ggc 624
 Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly
 195 200 205

atc ctg aag aag gaa aag gtc agc ctg ggc ggc gaa gac agc cgc gag 672
 Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu
 210 215 220

ggc ctg acc tgc gtg ctg tcg gtc 696
 Gly Leu Thr Cys Val Leu Ser Val
 225 230

<210> 16
 <211> 232
 <212> PRT
 <213> *Caulobacter crescentus*

<400> 16
 Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser
 1 5 10 15
 Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn
 20 25 30

Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser
 35 40 45
 Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala
 50 55 60
 Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp
 65 70 75 80
 Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu
 85 90 95
 Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp
 100 105 110
 His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly
 115 120 125
 Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu
 130 135 140
 Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp
 145 150 155 160
 Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe
 165 170 175
 Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe
 180 185 190
 Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly
 195 200 205
 Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu
 210 215 220
 Gly Leu Thr Cys Val Leu Ser Val
 225 230

<210> 17
 <211> 888
 <212> DNA
 <213> Pseudomonas putida

<220>
 <221> CDS
 <222> (1)...(888)

<400> 17
 ggc ggc ctg cac ggt gta ggc gtg tcg gta gtg aac gca ctg tct gaa 48
 Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu
 1 5 10 15
 gag ctc gtc ctc acc gtt cgc cgt agc ggc aag atc tgg gaa cag acc 96
 Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr
 20 25 30
 tac gtc cat ggt gtt ccg cag gaa ccg atg aag atc gtt ggc gac agc 144
 Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser
 35 40 45
 gaa acc acc ggc acc cag atc cac ttc aag gct tcc agc gaa acc ttc 192
 Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe
 50 55 60
 aag aac atc cac ttc agc tgg gac atc ctg gcc aag cgg att cgt gaa 240
 Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu
 65 70 75 80
 ctg tcc ttc ctc aac tcc ggt gtc ggc atc gtc ctc aag gat gag cgc 288
 Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg
 85 90 95

agc ggc aag gaa gaa ctg ttc aag tac gaa ggc ggc ttg cgc gcg ttc 336
 Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe
 100 105 110

gtt gaa tac ctg aac acc aac aag acc ccg gtc aac cag gtg ttc cat 384
 Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His
 115 120 125

ttc aac atc cag cgc gaa gac ggc atc ggc gta gaa atc gcc ctg cag 432
 Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln
 130 135 140

tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att 480
 Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
 145 150 155 160

ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg 528
 Pro Gln Arg Asp Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
 165 170 175

acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag 576
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
 180 185 190

cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg 624
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
 195 200 205

atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag 672
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
 210 215 220

gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg 720
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
 225 230 235 240

ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag 768
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
 245 250 255

ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg 816
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
 260 265 270

cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc 864
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
 275 280 285

ggc ctg ccg ggc aaa ctg gct gac 888
 Gly Leu Pro Gly Lys Leu Ala Asp
 290 295

<210> 18

<211> 296

<212> PRT

<213> Pseudomonas putida

<400> 18

Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu
 1 5 10 15
 Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr
 20 25 30

Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser
 35 40 45
 Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe
 50 55 60
 Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu
 65 70 75 80
 Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg
 85 90 95
 Ser Gly Lys Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe
 100 105 110
 Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His
 115 120 125
 Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln
 130 135 140
 Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
 145 150 155 160
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
 165 170 175
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
 180 185 190
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
 195 200 205
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
 210 215 220
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
 225 230 235 240
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
 245 250 255
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
 260 265 270
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
 275 280 285
 Gly Leu Pro Gly Lys Leu Ala Asp
 290 295

<210> 19
 <211> 531
 <212> DNA
 <213> Synechococcus sp.

<220>
 <221> CDS
 <222> (1)...(531)

<400> 19
 ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg aca ttg ccc ggt aaa 48
 Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys
 1 5 10 15
 tta gca gac tgt tcc agt cgc gat ccc ggt gaa tct gaa atc ttc atc 96
 Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile
 20 25 30
 gtg gaa ggg gat tcg gca ggt ggc agt gct aaa cag ggg cgc gat cgc 144
 Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg
 35 40 45
 cgc ttc caa gcc atc ctg cct ctg cgc ggc aaa atc ctc aac atc gag 192
 Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu
 50 55 60

aaa acg gac gat gcc aaa atc tac aaa aac act gag atc caa gcc ctg	240
Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu	
65 70 75 80	
att aca gcg ctg ggc ctc gga att aaa ggg gag gaa ttt gat gct tcc	288
Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser	
85 90 95	
caa ctg cgc tac cac cgt att gtg atc atg act gac gcg gac gtc gat	336
Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp	
100 105 110	
ggt gcg cac atc cgt acc ctc ttg ctc acc ttc ttc tat cgc tat cag	384
Gly Ala His Ile Arg Thr Leu Leu Thr Phe Phe Tyr Arg Tyr Gln	
115 120 125	
cga tcg ctg ctg gag cag ggc tac atg tac att gcc tgc ccg ccg ctg	432
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu	
130 135 140	
tac aag ttg gag cgg gga cgt aat cac tac tat tgc tac aac gaa cgc	480
Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg	
145 150 155 160	
gaa ctg cag gaa cgg att gcg acg ttc cct gaa aac gcc aac tat acg	528
Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr	
165 170 175	
att	531
Ile	

<210> 20
 <211> 177
 <212> PRT
 <213> Synechococcus sp.

<400> 20

Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys	
1 5 10 15	
Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile	
20 25 30	
Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg	
35 40 45	
Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu	
50 55 60	
Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu	
65 70 75 80	
Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser	
85 90 95	
Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp	
100 105 110	
Gly Ala His Ile Arg Thr Leu Leu Thr Phe Phe Tyr Arg Tyr Gln	
115 120 125	
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu	
130 135 140	
Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg	
145 150 155 160	
Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr	
165 170 175	
Ile	

<210> 21
 <211> 660
 <212> DNA
 <213> Caulobacter crescentus

<220>
 <221> CDS
 <222> (1)...(660)

<400> 21
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 Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
 1 5 10 15
 atc atc acc agc tac gcc gag agc tcc ggc atc ctg aag aag gaa aag 96
 Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
 20 25 30
 gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144
 Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
 35 40 45
 tgc gtc aag gtc ccg gat ccg aag ttc agc tgc cag acc aag gac aag 192
 Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
 50 55 60
 ctg gtc tgc tcc gaa gtg cgc ccc gcc gtt gag ggc ctg gtg tgc gaa 240
 Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
 65 70 75 80
 ggt ctc tgc acc tgg ttc gag gaa cat ccg aac gag gcc aag gcg atc 288
 Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile
 85 90 95
 gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag 336
 Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys
 100 105 110
 gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg 384
 Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu
 115 120 125
 ccc ggc aag ctc gcc gac tgc tgc gaa cgc gat ccg gcc aag tcc gag 432
 Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu
 130 135 140
 atc ttc atc gtc gag ggc gac tgc gcg ggc ggc tgc gcc aag cag gcc 480
 Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
 145 150 155 160
 cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc ggc aag atc ctg 528
 Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
 165 170 175
 aac gtc gag cgg gcc cgc ttc gac aag atg ctg tgc tcc gac cag atc 576
 Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
 180 185 190
 ggc acg ctg atc acc gcc ctg ggc gcg ggg atc ggc cgc gac gac ttc 624
 Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe
 195 200 205

aac ccg gac aag gtg cgc tac cac aag atc gtg ctg
Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu
210 215 220

660

<210> 22
<211> 220
<212> PRT
<213> Caulobacter crescentus

<400> 22
Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
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Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
20 25 30
Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
35 40 45
Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
50 55 60
Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
65 70 75 80
Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile
85 90 95
Val Thr Lys Ile Ala Glu Ala Ala Ala Arg Glu Ala Ala Arg Lys
100 105 110
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu
115 120 125
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu
130 135 140
Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
145 150 155 160
Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
165 170 175
Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
180 185 190
Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe
195 200 205
Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu
210 215 220

<210> 23
<211> 1422
<212> DNA
<213> Cytophaga lytica

<220>
<221> CDS
<222> (1)...(1422)

<400> 23
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Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
1 5 10 15
tct tgt gta aac gca tta tct aat aat tta aaa gct act gtt tac aga 96
Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg
20 25 30
gaa ggt aaa ata tgg gag caa gag tat gaa aga ggt aag gct tta tat 144
Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr
35 40 45

ccg gta aaa agt att gga gaa aca gag gaa aca ggt act ata gtt act	192
Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr	
50 55 60	
ttt tac cca gat gat act ata ttt aca caa act aca gag tat aat tat	240
Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr	
65 70 75 80	
gaa acg ctt tct aac aga atg cga gag ttg gct tac ctt aat aag gga	288
Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly	
85 90 95	
gtt aca att agc att aca gat aag aga gtt aaa gat gaa aag gga gag	336
Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu	
100 105 110	
ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att	384
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile	
115 120 125	
aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca	432
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser	
130 135 140	
atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac	480
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr	
145 150 155 160	
aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat	528
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn	
165 170 175	
aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca	576
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr	
180 185 190	
tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta	624
Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu	
195 200 205	
aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att	672
Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile	
210 215 220	
gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act	720
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr	
225 230 235 240	
aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca	768
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser	
245 250 255	
gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta	816
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val	
260 265 270	
att gta caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca	864
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr	
275 280 285	

aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt	912
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly	
290 295 300	
tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc	960
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys	
305 310 315 320	
gaa gta ttc ctt gta gag gga gat tgc gcg ggt ggt act gct aaa caa	1008
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln	
325 330 335	
ggg agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc	1056
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile	
340 345 350	
tta aat gtt gaa aaa gca atg caa cat aag gtt ttt gaa aac gaa gaa	1104
Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu	
355 360 365	
ata aaa aat att tac aca gct tta ggt gtt act att ggt aca gaa gaa	1152
Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu	
370 375 380	
gat agt aaa gcc tta aac tta gaa aaa tta aga tac cat aaa gta gtt	1200
Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val	
385 390 395 400	
att atg tgt gat gcc gat gta gat ggt agc cac att gaa act tta atc	1248
Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile	
405 410 415	
ctt aca ttc ttc ttc cgt ttt atg agg gag tta ata gaa ggc ggt cac	1296
Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His	
420 425 430	
gtt tat ata gca acc cca cct tta tac ttg gta aaa aag gga aca aaa	1344
Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys	
435 440 445	
aaa cgt tat gct tgg aat gat aaa gaa cga gat gag ata gca gaa agc	1392
Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser	
450 455 460	
ttt aat ggt agt gtt ggt ata caa aga tat	1422
Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr	
465 470	

<210> 24

<211> 474

<212> PRT

<213> Cytophaga lytica

<400> 24

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val	
1 5 10 15	
Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg	
20 25 30	
Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr	
35 40 45	
Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr	
50 55 60	

Phe	Tyr	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Gln	Thr	Thr	Glu	Tyr	Asn	Tyr
65					70				75						80
Glu	Thr	Leu	Ser	Asn	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly
				85					90					95	
Val	Thr	Ile	Ser	Ile	Thr	Asp	Lys	Arg	Val	Lys	Asp	Glu	Lys	Gly	Glu
			100					105					110		
Phe	Leu	Ser	Glu	Val	Phe	Tyr	Ser	Glu	Glu	Gly	Leu	Lys	Glu	Phe	Ile
	115						120					125			
Lys	Phe	Leu	Asp	Gly	Asn	Arg	Glu	Gln	Leu	Ile	Arg	Asp	Val	Val	Ser
	130					135					140				
Met	Glu	Gly	Glu	Lys	Asn	Gly	Ile	Pro	Val	Glu	Val	Ala	Met	Val	Tyr
145					150					155					160
Asn	Thr	Ser	Tyr	Ser	Glu	Asn	Leu	His	Ser	Tyr	Val	Asn	Asn	Ile	Asn
				165					170					175	
Thr	His	Glu	Gly	Gly	Thr	His	Leu	Ser	Gly	Phe	Arg	Arg	Gly	Leu	Thr
		180						185					190		
Ser	Thr	Leu	Lys	Lys	Tyr	Ala	Asp	Ala	Ser	Gly	Met	Leu	Asp	Lys	Leu
		195					200					205			
Lys	Phe	Glu	Ile	Gln	Gly	Asp	Asp	Phe	Arg	Glu	Gly	Leu	Thr	Ala	Ile
	210				215					220					
Val	Ser	Val	Lys	Val	Ala	Glu	Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr
225					230					235					240
Lys	Leu	Gly	Asn	Arg	Glu	Val	Ser	Ser	Ala	Val	Ser	Gln	Ala	Val	Ser
			245						250					255	
Glu	Met	Leu	Thr	Asn	Tyr	Leu	Glu	Glu	Asn	Pro	Asp	Asp	Ala	Lys	Val
			260					265					270		
Ile	Val	Gln	Lys	Val	Ile	Leu	Ala	Gln	Ala	Arg	His	Ala	Ala	Ala	Thr
		275					280					285			
Lys	Ala	Arg	Glu	Met	Val	Gln	Arg	Lys	Thr	Val	Met	Ser	Ile	Gly	Gly
	290					295				300					
Leu	Pro	Gly	Lys	Leu	Ser	Asp	Cys	Ser	Glu	Gln	Asp	Ala	Thr	Lys	Cys
305					310					315					320
Glu	Val	Phe	Leu	Val	Glu	Gly	Asp	Ser	Ala	Gly	Gly	Thr	Ala	Lys	Gln
			325						330					335	
Gly	Arg	Asp	Arg	Asn	Phe	Gln	Ala	Ile	Leu	Pro	Leu	Arg	Gly	Lys	Ile
			340					345					350		
Leu	Asn	Val	Glu	Lys	Ala	Met	Gln	His	Lys	Val	Phe	Glu	Asn	Glu	Glu
		355					360					365			
Ile	Lys	Asn	Ile	Tyr	Thr	Ala	Leu	Gly	Val	Thr	Ile	Gly	Thr	Glu	Glu
	370					375					380				
Asp	Ser	Lys	Ala	Leu	Asn	Leu	Glu	Lys	Leu	Arg	Tyr	His	Lys	Val	Val
385					390					395					400
Ile	Met	Cys	Asp	Ala	Asp	Val	Asp	Gly	Ser	His	Ile	Glu	Thr	Leu	Ile
			405						410					415	
Leu	Thr	Phe	Phe	Phe	Arg	Phe	Met	Arg	Glu	Leu	Ile	Glu	Gly	Gly	His
			420					425					430		
Val	Tyr	Ile	Ala	Thr	Pro	Pro	Leu	Tyr	Leu	Val	Lys	Lys	Gly	Thr	Lys
		435					440					445			
Lys	Arg	Tyr	Ala	Trp	Asn	Asp	Lys	Glu	Arg	Asp	Glu	Ile	Ala	Glu	Ser
	450					455					460				
Phe	Asn	Gly	Ser	Val	Gly	Ile	Gln	Arg	Tyr						
465					470										

<210> 25

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated DNA

<400> 25
tgtaaaacga cggccagtca ygcngngngn aarttyga

38

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 26
His Ala Gly Gly Lys Phe Asp
1 5

<210> 27
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 27
ctgcgttcgt atatgagcnc crtcnacrtc ngcrtc

36

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 28
Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu
1 5 10

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 29
gaagtcacga tgaccgttct gcaygsnggn ggaarttyg g

41

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 30
Glu Val Leu Met Thr Val Leu His Ala Gly Gly Lys Phe Gly
1 5 10

<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 31
agcagggtac ggatgtgcga gccrtcnacr tngcrtcng tgat

44

<210> 32
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 32
Met Thr Asp Ala Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu
1 5 10 15

<210> 33
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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<400> 33
caggaaacag ctatgaccar rtgngtnccn cc

32

<210> 34
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
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<400> 34
Gly Gly Thr His Leu
1 5

<210> 35
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 35
gcaacgagat caacactcmn gargnggna cnca

34

<210> 36
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 36
Asn Asn Ile Asn Thr His Glu Gly Gly Thr His
1 5 10

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 37
Asn Asn Ile Asn Thr Pro Glu Gly Gly Thr His
1 5 10

<210> 38
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 38
tgtaaaacga cggccagtar yttknkyyttn gtytg

35

<210> 39
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 39
Gln Thr Lys Thr Lys Leu
1 5

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 40
Gln Thr Lys Asp Lys Leu
1 5

<210> 41
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 41
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<210> 42
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 42
Asp Ala Asp Val Asp Gly
1 5

<210> 43
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 43
ccatagctgc gtagcattca tytncnccnar nccytt 36

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 44
Lys Gly Leu Gly Glu Met Asn Ala Thr Gln Leu Trp
1 5 10

<210> 45
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<400> 45
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<210> 46
<211> 8
<212> PRT
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<220>
<223> Synthetically generated protein

<400> 46
Lys Arg Pro Ala Met Tyr Ile Gly
1 5

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 47
Lys Arg Pro Gly Met Tyr Ile Gly
1 5

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 48
tgtaaaacga cggccagtcc nccngcnsr tcnccttc

38

<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 49
Glu Gly Asp Ser Ala Gly Gly
1 5

<210> 50
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
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<400> 50
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39

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 51
Gln Leu Trp Glu Thr Thr Met
1 5

<210> 52
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 52
Gln Leu Trp Asp Thr Thr Met
1 5

<210> 53
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<400> 53
gaagtcacatca tgaccgttct gcaygcnggn ggnaarttyg a

41

<210> 54
<211> 14
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<213> Artificial Sequence

<220>
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<400> 54
Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp
1 5 10

<210> 55
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 55
Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asn
1 5 10

<210> 56
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 56
Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Glu
1 5 10

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 57
Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Lys
1 5 10

<210> 58
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 58
tgtaaaacga cggccagtgc nggrtcytty tcytgrca

38

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 59
Cys Gln Glu Lys Asp Pro Ala
1 5

<210> 60
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 60
gaagtcacga tgaccgttct gcaacnaaya ayathccnca

40

<210> 61
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 61
Thr Asn Asn Ile Pro Gln
1 5

<210> 62
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 62
tgtaaaacga cggccagtaa yttnggntcn ggnacytt

38

<210> 63
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 63
Lys Val Pro Asp Pro Lys Phe
1 5

<210> 64
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 64
Lys Val Pro Glu Pro Lys Phe
1 5

<210> 65
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated DNA

<400> 65
caggaaacag ctatgaccgc nmrmrnrgcn mgnga

35

<210> 66
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 66
Ala Arg Arg Ala Arg Glu
1 5

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 67
Ala Arg Lys Ala Arg Glu
1 5

<210> 68
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 68
Ala Lys Lys Ala Arg Glu
1 5

<210> 69
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at pos. 1 = Pro or Ser; Xaa at pos. 2 = Ala or Thr; Xaa at pos. 3 = Ala, Val or Leu; Xaa at pos. 4 = Glu or Asp; Xaa at pos. 5 = Val or Thr; Xaa at pos. 6 = Ile or Val; Xaa at pos. 7 = Met, Leu or Phe; Xaa at pos. 9 = Val, Gln or Ile; Xaa at pos. 17 = Asp or Gly; Xaa at pos. 18 = Asp, Gly, Asn or Ser; Xaa at pos. 19 = Ser, Lys, Gly, Asp or Asn

<400> 69
Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe
1 5 10 15
Xaa Xaa Xaa

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated protein

<400> 70
Gly Gly Thr His
1

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at position 1 = Ile or Leu; Xaa at position 10 = Ala or Ser

<400> 71
Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu
1 5 10 15

<210> 72
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at position 5 = Gly or Ala; Xaa at position 10 = Ser or Asp

<400> 72
Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr
1 5 10

<210> 73
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at position 2 = Thr or Pro; Xaa at position 3 = Lys or Asn; Xaa at position 4 = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73
Gln Xaa Xaa Xaa Lys Leu
1 5

<210> 74
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at position 1 = Tyr or Phe; Xaa at position 9 = Ala or Pro

<400> 74
Xaa Lys Gly Leu Gly Glu Met Asn Xaa
1 5

<210> 75
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synethetically generated protein

<400> 75
Val Glu Gly Asp Ser Ala Gly Gly Ser
1 5

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at positio 2 = His or Val; Xaa at position 6 = Gln or Lys

<400> 76
Lys Xaa Pro Asp Pro Xaa Phe
1 5

<210> 77
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaa at position 9 = Ser or Gln; Xaa at position 10 = Ser or Glu; Xaa at position 11 = Lys or Arg; Xaa at position 14 = Ala or Ser